AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph [0093] with the following rewritten paragraph:

— **[0093]** In the preferred embodiment, the subject RDP-58 peptides comprise one or more of the cytomodulating peptides disclosed in co-pending U.S. Patent Applications U.S.S.N 09/028,083 & U.S.S.N. 08/838,916 as well as corresponding International application WO 98/46633, the disclosures of which are expressly incorporated herein by reference. In an especially preferred embodiment, the RDP-58 peptide comprises the sequence Arg-nL-nL-nL-Arg-nL-nL-nL-Gly-Tyr (SEQ ID NO:1), where nL is norleucine and all amino acids other than glycine are the D-stereoisomer. —

Please replace the paragraph [0095] with the following rewritten paragraph:

— **[0095]** More particularly, the preferred RDP-58 peptides for use in the compositions and methods of the present invention comprise oligopeptides having the sequence B-X-X-X-B-X-X-X-J-Tyr (SEQ ID NO:2), where B is a basic amino acid, preferably Lys or Arg, particularly Arg on at least one position, preferably at both positions; J is Gly, B or an aliphatic hydrophobic amino acid of from 5 to 6 carbon atoms, particularly Gly or B; and X is an aliphatic or aromatic amino acid. In one embodiment, at least three X amino acid residues are the same non-polar aliphatic amino acid, preferably at least four are the same non-polar aliphatic amino acid, more preferably at least five are the same non-polar aliphatic amino acid, and most preferably, all are the same non-polar aliphatic amino acid. In a preferred embodiment, the non-polar aliphatic amino acids are of from 5 to 6 carbon atoms, particularly 6 carbon atoms, particularly the non-polar aliphatic amino acids Val, Ile, Leu, and nL. Thus, in some embodiments, X is any amino acid other than a charged aliphatic amino acid, and preferably any amino acid other than a polar aliphatic amino acid. —

Please replace the paragraph [0096] with the following rewritten paragraph:

— **[0096]** Of the six amino acids indicated by X in the B-X-X-X-B-X-X-X-J-Tyr (SEQ ID NO:2) peptide sequence, preferably at least 3 are aliphatic amino acids of from 5 to 6 carbon atoms, more preferably at least 4 are aliphatic amino acids of from 5 to 6 carbon atoms, most preferably at least 5 are aliphatic amino acids of 5-6 carbon atoms, more particularly 6 carbon atoms. In a preferred embodiment, the aliphatic amino acids are non-polar aliphatic amino acids of from 5 to 6 carbon atoms, particularly Val, Ile, Leu, and nL. The other amino acids may be other uncharged aliphatic amino acids, particularly non-polar aliphatic amino acids or aromatic amino acids. —

Please replace the paragraph [0097] with the following rewritten paragraph:

— **[0097]** Compositions of particular interest will include an RDP-58 peptide having the sequence:

Arg-U-X-X-Arg-X-X-X-J-Tyr (SEQ ID NO:3) —

Please replace the paragraph [0101] with the following rewritten paragraph:

— **[0101]** Exemplary RDP-58 peptides include the following:

bc #											Seq Id #
1	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:4
2	Arg	Val	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:5
3	Arg	Ile	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:6
4	Arg	Leu	Val	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:7
5	Arg	Leu	Ile	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:8
6	Arg	Leu	Leu	Val	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:9
7	Arg	Leu	Leu	Ile	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:10
8	Arg	Leu	Leu	Leu	Arg	Val	Leu	Leu	Gly	Tyr	SEQ ID NO:11
9	Arg	Leu	Leu	Leu	Arg	Ile	Leu	Leu	Gly	Tyr	SEQ ID NO:12
10	Arg	Leu	Leu	Leu	Arg	Leu	Val	Leu	Gly	Tyr	SEQ ID NO:13
11	Arg	Leu	Leu	Leu	Arg	Leu	Ile	Leu	Gly	Tyr	SEQ ID NO:14
12	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Val	Gly	Tyr	SEQ ID NO:15
13	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Ile	Gly	Tyr	SEQ ID NO:16
14	Arg	Trp	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:17
15	Arg	Leu	Trp	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:18
16	Arg	Leu	Leu	Trp	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:19
17	Arg	Leu	Leu	Leu	Arg	Trp	Leu	Leu	Gly	Tyr	SEQ ID NO:20
18	Arg	Leu	Leu	Leu	Arg	Leu	Trp	Leu	Gly	Tyr	SEQ ID NO:21
19	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Trp	Gly	Tyr	SEQ ID NO:22

20	Arg	Tyr	Leu	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:23
21	Arg	Leu	Tyr	Leu	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:24
22	Arg	Leu	Leu	Tyr	Arg	Leu	Leu	Leu	Gly	Tyr	SEQ ID NO:25
23	Arg	Leu	Leu	Leu	Arg	Tyr	Leu	Leu	Gly	Tyr	SEQ ID NO:26
24	Arg	Leu	Leu	Leu	Arg	Leu	Tyr	Leu	Gly	Tyr	SEQ ID NO:27
25	Arg	Leu	Leu	Leu	Arg	Leu	Leu	Tyr	Gly	Tyr	SEQ ID NO:28
1Nl	Arg	nL	nL	nL	Arg	nL	nL	nL	Gly	Tyr	SEQ ID NO:1

nL = norleucine —

Please replace the paragraph [0107] with the following rewritten paragraph:

— **[0107]** The peptides may also be in the form of oligomers, particularly dimers of the peptides, which may be head to head, tail to tail, or head to tail, there being not more than about 6 repeats of the peptide. The oligomer may contain one or more D-stereoisomer amino acids, up to all of the amino acids. The oligomers may or may not include linker sequences between the peptides. When linker sequences are used, suitable linkers include those comprising uncharged amino acids and (Gly)n, where n is 1-7, Gly-Ser (e.g., $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO:29) and $(GGGS)_n$ (SEQ ID NO:30), where n is at least 1), Gly-Ala, Ala-Ser, or other flexible linkers, as known in the art. Linkers of Gly or Gly-Ser may be used since these amino acids are relatively unstructured, which allows interaction of individual peptides with cellular target molecules and limits structural perturbations between peptides of the oligomer. —

Please replace the paragraph [0124] with the following rewritten paragraph:

— **[0124]** In a further aspect, the presentation sequence confers the ability to bind metal ions to generate a conformationally restricted secondary structure. Thus, for example, C2H2 zinc finger sequences are used. C2H2 sequences have two cysteines and two histidines placed such that a zinc ion is chelated. Zinc finger domains are known to occur independently in multiple zinc-finger peptides to form structurally independent, flexibly linked domains (see Nakaseko, Y. et al. *J. Mol. Biol.* 228: 619-636 (1992)). A general consensus sequence is (5 amino acids)-C-(2 to 3 amino acids)-C-(4 to 12 amino acids)-H-(3 amino acids)-H-(5 amino acids) (SEQ ID NO:31). A preferred example would be -FQCEEC-random peptide of 3 to 20 amino acids-HIRSHTG (SEQ ID NO:32). Similarly, CCHC boxes having a consensus sequence -C-(2 amino acids)-C-(4 to 20 random peptide)-H-(4 amino acids)-C- (SEQ ID NO:33) can be

used, (see Bavoso, A. et al. *Biochem. Biophys. Res. Commun.* 242: 385-389 (1998)). Other examples include (1) -VKCFNC-4 to 20 random amino acids-HTARNCR- (SEQ ID NO:34), based on the nucleocapsid protein P2; (2) a sequence modified from that of the naturally occurring zinc-binding peptide of the Lasp-1 LIM domain (Hammarstrom, A. et al. *Biochemistry* 35: 12723-32 (1996)); and (3) -MNPNCARCG-4 to 20 random amino acids-HKACF- (SEQ ID NO:35), based on the NMR structural ensemble 1ZFP (Hammarstrom et al., *supra*). —

Please replace the paragraph [0134] with the following rewritten paragraph:

— **[0134]** Fusion partners include linker or tethering sequences for linking the peptides and for presenting the peptides in an unhindered structure. As discussed above, useful linkers include glycine polymers (G)n where n is 1 to about 7, glycine-serine polymers (e.g., (GS)n, (GSGGS)n (SEQ ID NO:29) and (GGGS)n (SEQ ID NO:30), where n is at least 1), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers known in the art. Preferably, the linkers are glycine or glycine-serine polymers since these amino acids are relatively unstructured, hydrophilic, and are effective for joining segments of proteins and peptides. —

Please insert the enclosed 11-page text entitled "SEQUENCE LISTING" immediately preceding the claims.